

PLANT TO PLANT VARIABILITY IN GROWTH AND DEVELOPMENT OF CONVENTIONAL AND TRANSGENIC MAIZE HYBRIDS.

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INTRODUCTION

The introduction of genes in a parental maize line, to obtain single cross hybrids tolerant to biotic stresses, may affect plant-to-plant variability of the obtained transgenic hybrid, because of the potential linkage drag (Tanksley and Nelson, 1996). In this work we have analyzed plant-to-plant variability of different traits of traditional and transgenic single cross maize hybrids (Bt: maize genetically altered to express the bacterial Bt toxin; RR: Rond-up resistant maize, and stacked Bt and RR).

MATERIALS AND METHODS

• The conventional DK747 maize hybrid and the transgenic versions of this hybrid (DK747MG¹, DK747RR, DK747MGR) and the transgenic hybrids DK190MG¹, DK190MRR, DK190MGRR were cultivated at two plant population densities (6 and 12 plants per square meter, D6 and D12, respectively) without nutrients limitations and water restriction. Weeds and insects were adequately controlled. The experiment was repeated during 2008- 2009 (Exp1) and 2009- 2010 (Exp2).

• Individual plant biomass and phonological stages were recorded on 10 plants per plot along the cycle. Plant biomass was estimated using allometric models (Maddonni and Otegui, 2004) until plants were harvested at physiological maturity (PM). Plant growth rates (PGR) were estimated: **PGR**_v (PGR between V₃ and V₆); **PGR**_{ps} (pre- silking PGR, between V₆ and V₁₃); **PGR**_s (around silking PGR; -15 days R₁, R₁, R₁, +15 days). Similarly, ear growth rates (**EGR**_s) were estimated around silking. At PM kernel number per plant (**KNP**) was recorded. Means and coefficients of variation (CV, %) were compared with ANOVA, considering P<0,05 significant differences.

| RESULTS | | | | | | | | | | | | |
|-----------|---------------|-------------|-------------|-------------|----------------|------------|--------------|-----------|---------------|-----------|-------------|------------|
| | PGRv (g/ day) | | CV PGRv (%) | | PGRps (g/ day) | | CV PGRps (%) | | PGRs (g/ day) | | CV PGRs (%) | |
| | D6 | D12 | D6 | D12 | D6 | D12 | D6 | D12 | D6 | D12 | D6 | D12 |
| DK747 | 0,59 (abcd) | 0,36 (e) | 22,5 (cd) | 24,3 (bcd) | 4,44 (cd) | 2,35 (g) | 18,1 (ab) | 20,6 (ab) | 8,17 (ab) | 4,41 (f) | 14,2 (de) | 23,5 (abc) |
| DK747MG | 0,62 (abc) | 0,45 (cde) | 19,4 (d) | 21,3 (d) | 4,50 (cd) | 2,84 (efg) | 15,2 (b) | 20,3 (ab) | 7,58 (cd) | 4,42 (f) | 14,3 (de) | 19,1 (bcd) |
| DK747RR | 0,59 (abcd) | 0,38 (e) | 26,4 (bcd) | 27,5 (bcd) | 4,21 (d) | 2,42 (fg) | 19,9 (ab) | 22,9 (a) | 8,72 (a) | 4,64 (f) | 12,6 (e) | 19,8 (bcd) |
| OK747MGRR | 0,68 (ab) | 0,36 (e) | 22,4 (cd) | 33,7 (ab) | 5,10 (ab) | 2,64 (fg) | 18,9 (ab) | 20,7 (ab) | 8,10 (bc) | 4,66 (f) | 12,6 (e) | 25,3 (ab) |
| DK190MG | 0,63 (abc) | 0,37 (e) | 28,8 (abcd) | 37,7 (a) | 4,79 (bc) | 2,84 (f) | 21,4 (a) | 22,1 (a) | 7,04 (de) | 3,67 (g) | 16,5 (de) | 18,9 (cde) |
| DK190RR | 0,66 (ab) | 0,43 (de) | 28,2 (abcd) | 24,5 (bcd) | 5,10 (ab) | 2,81 (fg) | 18,6 (ab) | 19,6 (ab) | 6,97 (e) | 3,83 (g) | 14,9 (de) | 16,1 (de) |
| OK190MGRR | 0,74 (a) | 0,61 (abcd) | 26,8 (bcd) | 28,1 (abcd) | 5,10 (ab) | 2,77 (g) | 20,1 (ab) | 22,0 (a) | 6,94 (e) | 4,19 (fg) | 17,4 (cde) | 18,5 (cde) |

Table 1: Mean values and CV of PGR_v, PGR_{ps} and PGR_s. For each column, different letters indicate significant differences among hybrids. Differences in PGR_{ps} and PGR_a among hybrids were found, mainly at D6. For example, DK747MGRR, DK190MGRR and DK190RR exhibited the highest PGR_w. Around silking, DK747MG exhibited the lowest PGR_v.



Figure 1: EGRs, KNP and CV of DK747 and the transgenic versions. Different letters indicate significant differences among them.

The DK747MGRR and DK747RR exhibited higher EGR_s than the other hybrids, especially at D12. Despite the higher EGR_s, no differences in kernel number were found among genotypes. The DK747 showed higher CV of KNP at D12.





Table 2: Thermal time (TT) to anthesis and silking, the anthesis- silking interval (ASI) and the partitioning index (PI:EGRs/PGRs). Different letters indicate significant differences among hybrids.

The DK747MGRR showed a shorter ASI than the other versions of DK747, especially at D12. The DK190MGRR had the same behavior, showing a smaller ASI at both densities. At D12 DK747MGRR, DK190RR and DK190MGRR exhibited the highest PI.



Figure 2: EGR₉, KNP and CV of DK190MG, DK190RR and DK190MGRR. Different letters indicate significant differences among hybrids.

DK190MGRR and DK190RR exhibited higher EGR_s at D12. Despite the higher EGR_s, no differences in KNP were found among genotypes. The DK190MG showed higher CV of KNP at D12.





Figure 5 and 6: Figure 5 shows the response of KNP to EGR₂. Lines represent the fitted function to the whole data set (both densities, both experiments), for each genotype. Figure 6 shows the reproductive efficiency (RE) at different EGR₂. Curves were obtained from fitted function of Fig. 5. Solid line represents the expected RE values at the explored EGR₃, while dotted line indicates the predicted RE for EGR not explored in our experiments. Note that DK190RR and 190MGRR exhibited lower ER values than DK190MGR EGR, with 1 and 3 g day¹.

CONCLUDING REMARKS AND FUTURE PROSPECTS

Differences in plant growth (PGRps, PGRs), ear growth around silking (EGR), and flowering phenology were found among versions of DK747 and DK190.

Despite of the higher EGRs of DK747MGRR, DK747RR, DK190MGRR and DK190RR, KNP was the same among the different versions, suggesting that the lower reproductive efficiency of the formers canceled the benefits of the higher EGRs to increase KNP

Considering that hybrids with the RR or the MGRR events showed a lower RE, we speculate that the RR event itself, or the linkage drag during its introduction in parental lines, reduces the reproductive efficiency of the obtained transgenic hybrids of DK747 and DK190. To understand the underlying processes of the lower RE of these transgenic hybrids, we will study the evolution of flower development and the synchrony of silks emergence of tested hybrids. Moreover, molecular markers will be used to find genetic differences among versions of both hybrids.

LITERATURE CITED

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